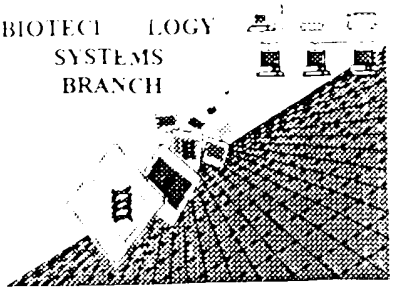
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/667,569

Source: OIPE

Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/667,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 _____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 _____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 _____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 _____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 _____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 _____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 _____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 _____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** 000
10 ✓	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 _____	Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.
12 _____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown". **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec 1.823 of new Rules)
13 _____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 05/07/2001
PATENT APPLICATION: US/09/667,569 TIME: 17:56:42

Input Set : A:\sequence.txt
Output Set: N:\CRF3\05072001\I667569.raw

Does Not Comply
Corrected Diskette Needed
pp. 1, 6

1 → Duplicate application number.

```
  3 <110> APPLICANT: Yocum, R. et al.
  5 <120> TITLE OF INVENTION: METHODS AND MICROORGANISMS FOR PRODUCTION OF
  6       PANTO-COMPOUNDS
  8 <130> FILE REFERENCE: BGI-141CP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/667,569
C--> 11 <141> CURRENT FILING DATE: 2000-09-21
 13 <150> PRIOR APPLICATION NUMBER: USSN 09/400,494
 14 <151> PRIOR FILING DATE: 1999-09-21
 16 <150> PRIOR APPLICATION NUMBER: USSN 60/210,072
 17 <151> PRIOR FILING DATE: 2000-06-07
 19 <150> PRIOR APPLICATION NUMBER: USSN 60/221,836
 20 <151> PRIOR FILING DATE: 2000-07-28
W--> 22 <150> PRIOR APPLICATION NO: USSN 60/221,838
 23 <151> PRIOR FILING DATE: 2000-08-24
 25 <160> NUMBER OF SEQ ID NOS: 94
 27 <170> SOFTWARE: PatentIn Ver. 2.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 311
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Haemophilus influenzae
 34 <400> SEQUENCE: 1
 35 Met Glu Phe Ser Thr Gln Gln Thr Pro Phe Leu Ser Phe Asn Arg Glu
 36   1               5                  10                  15
 38 Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln
 39              20                  25                  30
 41 Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu
 42          35                  40                  45
 44 Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile
 45      50                  55                  60
 47 Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg
 48  65                  70                  75                  80
 50 Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala
 51                  85                  90                  95
 53 Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His
 54             100                 105                 110
 56 Trp Pro Thr Glu Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu
 57         115                 120                 125
 59 Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
 60     130                 135                 140
 62 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 63 145                 150                 155                 160
 65 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 66                 165                 170                 175
 68 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 69             180                 185                 190
 71 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 72         195                 200                 205
```

RAW SEQUENCE LISTING DATE: 05/07/2001
PATENT APPLICATION: US/09/667,569 TIME: 17:56:42

Input Set : A:\sequence.txt
Output Set: N:\CRF3\05072001\I667569.raw

```
74 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
75     210                 215                 220
77 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
78 225                 230                 235                 240
80 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
81                 245                 250                 255
83 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
84             260                 265                 270
86 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
87         275                 280                 285
89 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
90     290                 295                 300
92 Glu Leu Ile Lys Leu Arg Lys
93 305                 310
96 <210> SEQ ID NO  2
97 <211> LENGTH  316
98 <212> TYPE: PRT
99 <213> ORGANISM  Escherichia coli
101 <400> SEQUENCE  2
102 Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp
103   1               5                  10                  15
105 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
106             20                  25                  30
108 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
109         35                  40                  45
111 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
112     50                  55                  60
114 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu
115 65                  70                  75                  80
117 Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
118                 85                  90                  95
120 Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
121             100                 105                 110
123 Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
124         115                 120                 125
126 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
127     130                 135                 140
129 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
130 145                 150                 155                 160
132 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
133                 165                 170                 175
135 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
136             180                 185                 190
138 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
139         195                 200                 205
141 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
142     210                 215                 220
144 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
145 225                 230                 235                 240
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RAW SEQUENCE LISTING DATE 05/07/2001
PATENT APPLICATION: US/09/667,569 TIME 17:56:42

Input Set : A:\sequence.txt
Output Set: N:\CRF3\05072001\I667569.raw

```
147 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
148                 245                 250                 255
150 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
151             260                 265                 270
153 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
154         275                 280                 285
156 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
157     290                 295                 300
159 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
160 305                 310                 315
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 319
165 <212> TYPE: PRT
166 <213> ORGANISM: Bacillus subtilis
168 <400> SEQUENCE: 3
169 Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
170   1               5                  10                  15
172 Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
173             20                  25                  30
175 Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
176         35                  40                  45
178 Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
179     50                  55                  60
181 His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
182 65                  70                  75                  80
184 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
185                 85                  90                  95
187 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
188             100                 105                 110
190 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
191         115                 120                 125
193 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
194     130                 135                 140
196 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
197 145                 150                 155                 160
199 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
200                 165                 170                 175
202 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
203             180                 185                 190
205 Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
206         195                 200                 205
208 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
209     210                 215                 220
211 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
212 225                 230                 235                 240
214 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
215                 245                 250                 255
217 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
218             260                 265                 270
```

RAW SEQUENCE LISTING DATE: 05/07/2001
PATENT APPLICATION: US/09/667,569 TIME: 17:56:42

Input Set : A:\sequence.txt
Output Set: N:\CRF3\05072001\I667569.raw

```
220 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
221         275                 280                 285
223 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
224     290                 295                 300
226 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
227 305                 310                 315
230 <210> SEQ ID NO: 4
231 <211> LENGTH: 312
232 <212> TYPE: PRT
233 <213> ORGANISM: Mycobacterium leprae
235 <400> SEQUENCE: 4
236 Met Pro Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Lys
237   1               5                  10                  15
239 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
240             20                  25                  30
242 Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
243         35                  40                  45
245 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
246     50                  55                  60
248 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
249 65                  70                  75                  80
251 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
252                 85                  90                  95
254 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
255             100                 105                 110
257 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
258         115                 120                 125
260 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
261     130                 135                 140
263 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
264 145                 150                 155                 160
266 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
267                 165                 170                 175
269 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
270             180                 185                 190
272 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
273         195                 200                 205
275 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
276     210                 215                 220
278 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
279 225                 230                 235                 240
281 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
282                 245                 250                 255
284 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
285             260                 265                 270
287 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
288         275                 280                 285
290 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
291     290                 295                 300
```

RAW SEQUENCE LISTING DATE: 05/07/2001
PATENT APPLICATION: US/09/667,569 TIME: 17:56:42

Input Set A:\sequence.txt
Output Set N:\CRF3\05072001\I667569.raw

293 Asn Arg Leu Arg Leu Arg Lys Leu
294 305 310
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 312
299 <212> TYPE: PRT
300 <213> ORGANISM: Mycobacterium tuberculosis
302 <400> SEQUENCE: 5
303 Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
304 1 5 10 15
306 Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
307 20 25 30
309 Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
310 35 40 45
312 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
313 50 55 60
315 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
316 65 70 75 80
318 Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
319 85 90 95
321 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
322 100 105 110
324 Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
325 115 120 125
327 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
328 130 135 140
330 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
331 145 150 155 160
333 Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
334 165 170 175
336 Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
337 180 185 190
339 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
340 195 200 205
342 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
343 210 215 220
345 Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
346 225 230 235 240
348 Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
349 245 250 255
351 Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile
352 260 265 270
354 Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
355 275 280 285
357 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
358 290 295 300
360 Asn Arg Leu Arg Leu Arg Lys Leu
361 305 310
364 <210> SEQ ID NO: 6
365 <211> LENGTH: 329

09/667,564

p 6

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 45
ttaagaaagg aggtgannnn atg 23

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 46
ttagaaagga ggtgannnnn atg 23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 47
agaaaggagg tgannnnnnn atg 23

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 48
agaaaggagg tgannnnnna tg 22

* These sequences are missing the mandatory <220> + <223> feature to explain the "n's" in the sequences. See #10 on the Error

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/667,569**

DATE 05/07/2001
TIME 17:56:43

Input Set : **A:\sequence.txt**
Output Set: **N:\CRF3\05072001\I667569.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:288 W: Application Number is Repeated, <150> PRIOR APPLICATION NUMBER
L:2892 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2892 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2904 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2904 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2918 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47
L:2918 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:2918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:2930 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:2930 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:7767 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88
L:7767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88
L:7767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88